



SEQUENCE LISTING

<110> LEWIN, DAVID A.
PENNICA, DIANE
RASTELLI, LUCA
TALLION, BRUCE

<120> WNT-REGULATED CYTOKINE-LIKE POLYPEPTIDE AND NUCLEIC
ACIDS ENCODING SAME

<130> 11669.191USU1

<140> 09/715,418

<141> 2000-11-16

<150> 60/166,177

<151> 1999-11-18

<160> 49

<170> PatentIn Ver. 2.1

<210> 1

<211> 212

<212> DNA

<213> Mus sp.

<400> 1

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tgtaatgact cgaaactgga gtttgaagc tt 212
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<210> 2

<211> 1670

<212> DNA

<213> Mus sp.

<220>

<221> misc_feature

<222> (1541)

<223> "n" represents a, t, c, g, other or unknown

<400> 2

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<210> 3
 <211> 131
 <212> PRT
 <213> Mus sp.

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<400> 3
Ser Ile Ser Ser Cys Gly Ala Gly Tyr Arg Thr Asp Asp Lys Thr Gln
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Leu Thr Glu Gly Arg Thr Ser Val Pro Gly Thr Met Gly Gln Cys Arg
      20             25             30

Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val Glu Arg Ala
    35             40             45

Ile Glu Thr Leu Ile Lys Asn Phe His Lys Tyr Ser Val Ala Gly Lys
    50             55             60

Lys Glu Thr Leu Thr Pro Ala Glu Leu Arg Asp Leu Val Thr Gln Gln
    65             70             75             80

Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala
      85             90             95

Asn Leu Gly Asn Cys Asn Asp Ser Lys Leu Glu Phe Gly Ser Phe Trp
    100            105            110

Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Met Glu Arg Pro Val
    115            120            125

Thr Arg Ser
    130

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<210> 4
 <211> 357
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> "n" represents a, t, c, g, other or unknown

<220>

<221> misc_feature

<222> (337)

<223> "n" represents a, t, c, g, other or unknown

<400> 4

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catcaagaac tttcaccagt actccgtgga ggggtgggaag gagacgctga ccccttctga 180
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agagaaaatt gccaacctgg gcagctgcaa tgactctaaa ctggagttca ggagtttctg 300
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<210> 5

<211> 379

<212> DNA

<213> Homo sapiens

<400> 5

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caggttgcca attttctctt ccaggccaca gttgctcggc atgagatggg gcagctgctg 180
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ctggtgaaag ttcttgatga gggctctaat ggccctctcc acatcactga attcctgagc 300
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gagagttctg ttgtcctat 379
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<210> 6

<211> 118

<212> PRT

<213> Homo sapiens

<400> 6

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Asp Asn Arg Thr Leu Thr Lys Gly Pro Asp Thr Val Ser Thr Met Gly
  1             5             10             15

Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val
          20             25             30

Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val
          35             40             45

Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val
          50             55             60

Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu
  65             70             75             80
```

Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg
85 90 95

Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Leu Glu
100 105 110

Arg Pro Val Arg Gly His
115

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
cttgatgagg gtctcaatgg 20

<210> 8
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 8
ccacatcact gaattcctga gcatcc 26

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
cagacacagt gagcaccatg 20

<210> 10
<211> 98
<212> PRT
<213> Homo sapiens, W27152, chemotactic cytokine II CCII from WO97/34013

<400> 10
Met Ala Ala Glu Pro Leu Thr Glu Leu Glu Glu Ser Ile Glu Thr Val
1 5 10 15

Val Thr Thr Phe Phe Thr Phe Ala Arg Gln Glu Gly Arg Lys Asp Ser
 20 25 30
 Leu Ser Val Asn Glu Phe Lys Glu Leu Val Thr Gln Gln Leu Pro His
 35 40 45
 Leu Leu Lys Asp Val Gly Ser Leu Asp Glu Lys Met Lys Ser Leu Asp
 50 55 60
 Val Asn Gln Asp Ser Glu Leu Lys Phe Asn Glu Tyr Trp Arg Leu Ile
 65 70 75 80
 Gly Glu Leu Ala Lys Glu Ile Arg Lys Lys Lys Asp Leu Lys Ile Arg
 85 90 95
 Lys Lys

<210> 11
 <211> 110
 <212> PRT
 <213> Homo sapiens, G491246, Macrophage Migration Inhibition Factor (MRP-14)

<400> 11
 Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile Asn Thr Phe His
 1 5 10 15
 Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu Asn Gln Gly Glu
 20 25 30
 Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe Leu Lys Lys Glu
 35 40 45
 Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu Asp Leu Asp Thr
 50 55 60
 Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile Met Leu Met Ala
 65 70 75 80
 Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu Gly Asp Glu Gly
 85 90 95
 Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly Thr Pro
 100 105 110

<210> 12
 <211> 37
 <212> PRT
 <213> Unknown Organism
 <220>
 <223> Description of Unknown Organism: 3-100/ICaBP type
 calcium binding protein

<400> 12

Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn
1 5 10 15

Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala
20 25 30

Ala Lys Ser Val Lys
35

<210> 13

<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 3-100/ICaBP type
calcium binding protein

<400> 13

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
1 5 10 15

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp
20 25 30

Leu Val Thr Gln Gln
35

<210> 14

<211> 19

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Bacterial type II
secretion system protein F

<400> 14

Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu
1 5 10 15

Glu Lys Ile

<210> 15

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Ubiquitin
carboxyl-terminal hydrolases family

<400> 15
 Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
 1 5 10

<210> 16
 <211> 49
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Bacterial
 themotaxis sensory transducers protein

<400> 16
 Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr
 1 5 10 15

 Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
 20 25 30

 Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
 35 40 45

 Phe

<210> 17
 <211> 32
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism:
 Phosphoenolpyruvate carboxykinase (ATP) protein

<400> 17
 Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
 1 5 10 15

 Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
 20 25 30

<210> 18
 <211> 33
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Prokaryotic-type
 carbonic anhydrases proteins

<400> 18

His Gln Tyr Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu
 1 5 10 15

Leu Arg Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn
 20 25 30

Cys

<210> 19

<211> 15

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Ergosterol
 biosynthesis ERG4/ERG24 family protein

<400> 19

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg
 1 5 10 15

<210> 20

<211> 25

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:
 Lysosome-associated membrane glycoproteins du

<400> 20

Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly
 1 5 10 15

Ser Cys Asn Asp Ser Lys Ile Glu Phe
 20 25

<210> 21

<211> 39

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:
 Phosphofructokinase proteins

<400> 21

Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys
 1 5 10 15

Asn Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu
 20 25 30

Ala Ala Lys Ser Val Lys Leu
35

<210> 22
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: PH domain
proteins profile

<400> 22
Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile
1 5 10

<210> 23
<211> 45
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Myotoxins
protein

<400> 23
Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
1 5 10 15

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
20 25 30

Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
35 40 45

<210> 24
<211> 17
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Phosphatidylinositol-specific phospholipase X

<400> 24
Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser
1 5 10 15

Cys

<210> 25
<211> 45

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Glypicans
protein

<400> 25

Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu
35 40 45

<210> 26

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Membrane attack
complex components/perforin

<400> 26

Ile Lys Asn Phe His Gln Tyr Ser Val Glu
1 5 10

<210> 27

<211> 44

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Urease nickel
ligands protein

<400> 27

Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly Lys Glu
1 5 10 15

Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln Leu Pro
20 25 30

His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
35 40

<210> 28

<211> 13

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phosphoglycerate
mutase family phosphohistidi

<400> 28

Gln Glu Phe Ser Asp Val Glu Arg Ala Ile Glu Thr Leu
1 5 10

<210> 29

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Ribosomal protein
L23 protein

<400> 29

Glu Leu Arg Asp Leu Val Thr Gln Gln Leu
1 5 10

<210> 30

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:
2'-5'-oligoadenylate synthetases protein

<400> 30

Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu
1 5 10 15

Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val
20 25 30

Lys Leu Glu Arg Pro Val Arg Gly His
35 40

<210> 31

<211> 24

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Formate and
nitrite transporters protein

<400> 31

Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly
1 5 10 15

Leu Glu Glu Lys Ile Ala Asn Leu
20

<210> 32

<211> 34

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Glycoprotein
hormones beta chain protein

<400> 32

Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp
1 5 10 15

Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser
20 25 30

Val Glu

<210> 33

<211> 21

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Vinculin family
talin-binding region protein

<400> 33

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln
1 5 10 15

Leu Pro His Leu Met
20

<210> 34

<211> 40

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Beta-lactamases
clas B protein

<400> 34

Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly
1 5 10 15

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln
12

20 25 30

Leu Pro His Leu Met Pro Ser Asn
35 40

<210> 35
<211> 21
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Heat shock hsp20
protein family profile

<400> 35
Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser
1 5 10 15

Val Lys Leu Glu Arg
20

<210> 36
<211> 35
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Hydroxymethylglutaryl-coenzyme A lyase protein

<400> 36
Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

Ser Val Glu
35

<210> 37
<211> 294
<212> DNA
<213> Mus sp.

<400> 37
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ggtgaccagg tcccgtagct cagaaggggt cagcgtctcc ttcccaccct ccacggagta 240
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<210> 38
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 38
 Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser
 1 5 10 15
 Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu
 20 25 30
 Val Thr Gln Gln Leu Pro His Leu Met Pro Ser
 35 40

<210> 39
 <211> 104
 <212> PRT
 <213> Homo sapiens translation of GenBank Accession AAY007220

<400> 39
 Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
 1 5 10 15
 Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
 20 25 30
 Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp
 35 40 45
 Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu
 50 55 60
 Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu
 65 70 75 80
 Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
 85 90 95
 Leu Glu Arg Pro Val Arg Gly His
 100

<210> 40
 <211> 94
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 40

Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
 1 5 10 15
 Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Tyr Ser
 20 25 30
 Val Gly Lys Glu Thr Leu Thr Pro Glu Leu Arg Asp Leu Val Thr Gln
 35 40 45
 Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile
 50 55 60
 Ala Asn Leu Gly Cys Asn Asp Ser Lys Leu Glu Phe Ser Phe Trp Glu
 65 70 75 80
 Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Glu Arg Pro Val
 85 90

<210> 41
 <211> 41
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: gi/4139958/pdb/1MHO

<400> 41
 Glu Lys Ala Val Val Ala Leu Ile Asp Val Phe His Gln Tyr Ser Gly
 1 5 10 15
 Arg Glu Gly Asp Lys His Lys Leu Lys Lys Ser Glu Leu Lys Glu Leu
 20 25 30
 Ile Asn Asn Glu Leu Ser His Phe Leu
 35 40

<210> 42
 <211> 41
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Protein MRP-126

<400> 42
 Glu Lys Ala Ile Asp Val Ile Ile Asp Val Phe His Gln Tyr Ser Arg
 1 5 10 15
 Arg Glu Gly Asp Lys Asp Thr Leu Thr Arg Lys Glu Leu Lys Leu Leu
 20 25 30
 Ile Glu Lys Gln Leu Ala Asn Tyr Leu
 35 40

<210> 43
<211> 41
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: ICTACALCIN

<400> 43
Gln Lys Gly Met Ala Leu Leu Ile Ser Thr Phe His Lys Tyr Ser Gly
1 5 10 15
Lys Glu Gly Asp Lys Cys Thr Leu Thr Lys Gly Glu Leu Lys Asp Leu
20 25 30
Ile Thr Lys Glu Leu Gly Gly Ala Phe
35 40

<210> 44
<211> 41
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: CALGRANULIN B

<400> 44
Glu Ser Ser Ile Glu Thr Ile Ile Asn Ile Phe His Gln Tyr Ser Val
1 5 10 15
Arg Leu Gly His Tyr Asp Thr Leu Ile Gln Lys Glu Phe Lys Gln Leu
20 25 30
Val Gln Lys Glu Leu Pro Asn Phe Leu
35 40

<210> 45
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 45
Ile Phe His Tyr Ser Gly Leu Glu Leu Leu
1 5 10

<210> 46
<211> 41
<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: CALGRANULIN B

<400> 46

Glu	Arg	Ser	Ile	Thr	Thr	Ile	Ile	Asp	Thr	Phe	His	Gln	Tyr	Ser	Arg
1				5				10					15		

Lys	Glu	Gly	His	Pro	Asp	Thr	Leu	Ser	Lys	Lys	Glu	Phe	Arg	Gln	Met
			20				25						30		

Val	Glu	Ala	Gln	Leu	Ala	Thr	Phe	Met
		35					40	

<210> 47

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus sequence

<400> 47

Glu	Ile	Phe	His	Gln	Tyr	Ser	Gly	Leu	Glu	Leu
1				5				10		

<210> 48

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Unknown Organism: reverse strand sequence of SEQ ID NO:4 (GenBank AA315020)

<220>

<221> misc_feature

<222> (21)..(21)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (127)..(127)

<223> n is a, c, g, or t

<400> 48

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aggccanagt	tgctcggcac	gagatggggc	agctgctggg	tgaccaggtc	ccgtagctca	180
gaaggggtca	gcgtctcctt	cccaccctcc	acggagtact	ggtgaaagtt	cttgatgagg	240
gtctcaatgg	ccctctccac	atcactgaat	tcctgagcat	cctctgcgtt	ggctgaccga	300
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<210> 49
 <211> 104
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 49

Met	Gly	Gln	Cys	Arg	Ser	Ala	Asn	Ala	Glu	Asp	Ala	Gln	Glu	Phe	Ser	1	5	10	15
Asp	Val	Glu	Arg	Ala	Ile	Glu	Thr	Leu	Ile	Lys	Asn	Phe	His	Gln	Tyr	20	25	30	
Ser	Val	Glu	Gly	Gly	Lys	Glu	Thr	Leu	Thr	Pro	Ser	Glu	Leu	Arg	Asp	35	40	45	
Leu	Val	Thr	Gln	Gln	Leu	Pro	His	Leu	Met	Pro	Ser	Asn	Cys	Gly	Leu	50	55	60	
Glu	Glu	Lys	Ile	Ala	Asn	Leu	Gly	Ser	Cys	Asn	Asp	Ser	Lys	Leu	Glu	65	70	75	80
Phe	Arg	Ser	Phe	Trp	Glu	Leu	Ile	Gly	Glu	Ala	Ala	Lys	Ser	Val	Lys	85	90	95	
Leu	Glu	Arg	Pro	Val	Arg	Gly	His									100			